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Nationwide survey of Hepatitis E virus infection in pigs in Thailand: only genotype 3 is endemic

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Background: Hepatitis E virus (HEV) infection in pigs is endemic in both developed and developing countries. Most of swine HEV isolated so far belong to genotype 3 or 4. Several studies proposed that genotype 3 and 4 are freely transmissible between human and swine. To assess the potential source of infection attributable to swine farming, we analyzed the prevalence of naturally infection pigs in Thailand.

Methods: During the period between May 2008 and June 2009, total 532 pig feces were collected from pig farms in different age of pigs, 1 to 6 month-old, sows, and boars, within 6 regions of Thailand, central, eastern, western, northern, upper north-eastern, and lower north-eastern. The specimens were tested for HEV RNA by semi-nested RT-PCR using universal primers. All positive samples were directly sequenced and 415 bp nucleotide sequences were compared with known HEV strains from GenBank.

Results: Overall, 112 (21.1%) out of 532 fecal samples were detected HEV RNA. The prevalence of HEV infection of all areas and groups ranged from 0.0-29.2% and 0.2-4.5%, respectively. The highest prevalence was in the upper north-eastern area. However, if both parts of north-eastern were combined (21.6%), the highest prevalence was the western area with of the most pig farming zone of Thailand (28.2%). Sequence analysis revealed that swine HEV isolates from Thailand were clustered into genotype 3 of HEV.

Conclusion: In this study, we showed the relatively high prevalence rate of HEV infection in swine in Thailand that seem to be contrast with the rarity case of clinical hepatitis E in Thai population. HEV genotype 3 become a new risk and is considered as viral zoonosis by reason of several reports of human cases worldwide, including Thailand.

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Prevalence and seasonality of Salmonella isolations from commercial poultry in Zaria Nigeria: a five-year retrospective study

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Background: Salmonellosis in poultry is caused by *Salmonella enterica* subspecie *enterica* serovar *Gallinarum* biovar *Gallinarum* (*Salmonella* Gallinarum) and biovar *Pullorum* (*Salmonella* Pullorum) responsible for Fowl Typhoid and Pullorum Disease respectively. In Africa, these diseases are of particular economic importance especially in such countries with expanding poultry industry, as Nigeria.

Methods: To determine the prevalence and seasonality of *Salmonella* isolations from commercial poultry, a retrospective analysis of laboratory-confirmed cases of avian salmonellosis was conducted from 2006-2010 records of poultry diseases reported in Zaria, Nigeria.

Results: A prevalence of 18.7% (334 cases) was recorded out of 1,783 outbreaks of poultry diseases. Avian salmonellosis occurred throughout the year in Zaria, with high incidence during the rainy season. *Salmonella* was observed to be 7 times more likely to be isolated from farms with flocks of 5,000 or more birds and the risk of isolation was shown to be 1.5 more from layers than either broilers or pullets/cockerels.

Conclusion: It is recommended that farmers should be encouraged to improve biosecurity and hygiene especially in layer farms with large flocks.

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Zoonotic surveillance for Rickettsiae in domestic animals in Kenya

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Background: Rickettsiae are obligate intracellular bacteria that cause zoonotic and human diseases. Arthropod vectors such as

fleas, mites, ticks and lice transmit rickettsiae to vertebrates during blood meals. In humans, the disease can be life threatening. This study was conducted amidst rising reports of rickettsioses among travelers to Kenya.

Methods: Ticks and whole blood were collected from domestic animals presented for slaughter at major slaughter houses in Nairobi and Mombasa that receive animals from nearly all districts in the country. Blood samples and ticks were collected from 1,019 cattle, 379 goats and 299 sheep and were screened for rickettsiae by a qPCR assay (Rick17b) using primers and probe that target the genus specific 17kDa gene (htrA). The ticks were identified using standard taxonomic keys. All Rick17b positive tick DNA samples were amplified and sequenced with primers sets that target rickettsial outer membrane protein genes (ompA and ompB) and the citrate-synthase encoding gene (gltA).

Results: Using the Rick17b qPCR, rickettsial infections in domestic animals were found in 31/42 districts sampled (73.8% prevalence). Infection rates were comparable in cattle (16.3%) and sheep (15.1%) and but were lower in goats (7.1%). Of the 596 ticks collected, 139 had rickettsiae (23.3%), and the detection rates were highest in Amblyomma (62.3%; n = 104) then Rhipicephalus (45.5%; n = 120), Hyalomma (35.9%; n = 28) and Boophilus (34.9%; n = 30). Following sequencing, 30 tick DNA samples had good reverse and forward sequences for the three target genes. On querying GenBank with the generated consensus sequences, homologies of 93-100% for the following spotted fever group (SFG) rickettsiae were identified: Rickettsia africae (86.7%, n = 26), Rickettsia aeschlimannii (3.3%, n = 1), Rickettsia mongolotimonae (3.3%, n = 1), Rickettsia conorii subsp. israelensis (3.3%, n = 1) and Candidatus Rickettsia kulagini (3.3%).

Conclusion: Molecular methods were used in this study to detect and identify rickettsial infections in domestic animals and ticks throughoutKenya.

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Integration of informal waste pickers in dengue fever control partnerships in Rio de Janeiro, Brazil

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Background: Dengue control campaigns in Rio de Janiero recruited *catadores*, or informal waste pickers, in interventions that aimed to reduce mosquito vector reservoirs by collecting refuse in slums patrolled by Unidades de Polícia Pacificadora (UPPs), or 'pacification' police. This medical anthropological study investigated the political and epidemiological significance of efforts to conjoin vector control, social control and social inclusion. Based on the premise that effective integration of a range of social actors is crucial to important yet neglected dengue control initiatives, this study hypothesized that: (H1) if catadores worked within cooperatives (coops), then catador participation in dengue partnerships would be greater than if catadores worked autonmously; and (H2) if surveillance data showed reductions in *Aedes aegypti* infestations following interventions that deployed catadores, then dengue interventions that include catadores would expand to slums not yet 'pacificed' by UPPs.

Methods: Data was collected and analyzed from June 2011 to February 2012. The city of Rio de Janeiro was mapped to identify locations where catadores worked autonomously or as members of coops, and sites of political activism where catadores demanded that society recognize the informal waste labor sector as legitimate. Surveys recruited an initial sample of catadores (N = 80). Respondent-driven sampling identified a final cohort (N = 30) stratified by catadores categorized as: autonomous/politically active (n = 5); autonomous/not politically active (n = 5); coop-member/politically active (n = 10); coop-member/not politically active (n = 10). Semi-structured interviews interrogated attitudes and behaviors regarding civil-state partnerships. Ethnographic participant-observation investigated cultural beliefs about 'pacification' policing that informants did not always openly speak about. State-published data was used to analyze variance in vector infestation rates at 19 intervention sites.

Results: 40% of respondents who participated in interventions held coop membership. 50% of catadores who participated in civil-state intervention partnerships identified themselves as politically active; 85% of this group exhibited distrust of police and perceived civil-state partnerships to undermine catador politics. Vector indices declined at all sites during the study, but interventions that included catadores did not expand beyond slums with UPPs.

Conclusion: Informal waste pickers contributed to effective dengue vector control in slums where 'pacification' police units secured state access. However, scale-up of socially inclusive dengue campaigns may depend on developing civil-state partnerships in areas where UPPs do not operate.

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Dietary lactobacillus down-regulated inflammatory pathway and maintained antioxidant status in collagen induced arthritic wistar rats

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Background: *Lactobacillus* species have been in use as a model probiotic. They are used as dietary supplement for their immunomodulatory nature. *in vitro* antioxidant nature and radical scavenging property of *Lactobacillus* species are well known. In a view of the well established immunomodulatory property of *Lactobacillus*, present investigation was carried out to evaluate the antioxidant and anti-inflammatory potential of *L. casei a*nd *L. acidophilus*, against inflammatory pathway and oxidative stress developed in arthritis induced by collagen and freund's incomplete adjuvant.

Methods: Collagen induced arthritis (CIA) model was used by injecting collagen and freund's incomplete adjuvant on day 1st on back of Wistar rats. On day 7th booster dose was given on tail. Oral administration of 2X10 8 CFU/ml of *L. casei* and *L. acidophilus* started from day 1st up to 28th day. Indomethacin was used at standard